

## FIG. 1A

1 ACCTGAGTAA GAGCTTGGA AAGTTGAGCC CTCCTCGAGA GAAATTGGAA GAACAGTTTA AGAGGCTGCT ATTCCAAAAA GCTTTCAACT CTCAGCAGTT  
 TGGACTCAIT CTCGAACCTT TTCAAACTCG GAGAAGCTCT CTTTAACTT TCTCCGACGA TAAGGTTTTT CGAAAGTTGA GAGTCGTCAA

101 AGTTCATGTC ATTGTCATTA ACCTGTTTCA ACTTCATCAC CTTCGTGACT TTAGCAATGA AACCGAGCAG CACACTTATA GCCAAGATGA GCAGCTATGT  
 TCAAGTACAG TAACAGTAAT TGGACAAAGT TGAAGTAGTG GAAGCACTGA AATCGTTACT TTGGCTCGTC GTGTGAATAT CGGTTCTACT CGTCGATACA

+3 MetSer PheLeuGlyIle LeuCysLys CysProLeu GlnAsnGluSer GlnGluGlu SerTyrAsn AlaTyrProLeu  
 -----  
 101 TGGACACAGT TGCTGGCCCT CTTTATGTC TTTCTTGGCA TCCTGTGCAA GTGTCCTCTA CAGAAAGAGT CTCAGGAGGA GTCTACAAT GCCTATCCTC  
 ACCTGTGTCA ACGACCGGGA GAAATACAGA AAAGAACCCT AGGACACGTT CACAGGAGAT GTCTTACTCA GAGTCCTCCT CAGGATGTTA CGGATAGGAG

+3 LeuProAlaVal LysValSer MetAspTrpLeu ArgLeuArg ProArgVal PheGlnGluAla ValValAsp GluArgGln TyrIleTrpPro TrpLeuIle  
 -----  
 101 TTCCAGCAGT CAAGTCTCC ATGGACTGCC TAAGACTCAG ACCCAGGTC TTTCCAGGAG CAGTGGTGA TGAAGACAG TACATTGGC CTGGTTGAT  
 AAGGTGTC GATCCAGAG TACCTGACCG ATTCTGAGTC TGGTCCCG AAGTCCTCC GTCCACCCT ACTTCTGTC ATGTAAACCG GGACCAACTA

+3 IleSerLeuLeu AsnSerPheHis ProHisGlu GluAspLeu SerSerIleSer AlaThrPro LeuProGlu GluPheGluLeu GlnGlyPhe LeuAlaLeu  
 -----  
 101 TTCTCTTCTG AATAGTTTCC ATCCCCATGA AGAGACCTC TCAAGTATTA GTGGACACCC ACTTCCAGAG GAGTTGAAT TACAAGGAT TTTGGCATTG  
 AAGAGAAGAC TTATCAAAAG TAGGGGTACT TCTCCTGGAG AGTTCATAAT CACGCTGTGG TGAAGGTCTC CTCAAAACCTA ATGTTCCCTAA AAACCGTAAC

+3 ArgProSerPhe ArgAsnLeu AspPheSer LysGlyHisGln GlyIleThr GlyAspLys GluGlyGlnGln ArgArgIle ArgGlnGln ArgLeuIleSer  
 -----  
 101 AGACCTTCTT TCAGGAACCTT GGATTTTTC AAAGTTCACC AGGGTATTAC AGGGACAAA GAAGGCCAGC AACACGAAT ACGACACAA CGCTTGATCT  
 TCTGGAAGAA AGTCCTTGAA CCTAAAAGG TTTCCAGTGG TCCCATATG TCCCTGTTT CTTCGGGTGG TTGCTGCTTA TGCTGTGCTT GCGAACTAGA

+3 SerIleGlyLys TrpIleAla AspAsnGlnPro ArgLeuIle GlnCysGlu AsnGluValGly LysLeuLeu PheIleThr GluIleProGlu LeuIleLeu  
 -----  
 601 CTATAGGCAA ATGGATTGCT GATAATCAGC CAAGGTGAT TCAGTGTGAA AATAGGTAG GAAATTTGTT GTTTATCACA GAAATCCAG AATTAATACT  
 GATATCCGTT TACCTAACGA CTATTAGTC GTTCCGACTA AGTCACACTT TTACTCCATC CCTTTAACAA CAATAGTGT CTTTAGGCTC TTAATTATGA

+3 LeuGluAspPro SerGluAlaLys GluAsnLeu IleuGln GluThrSerVal IleGluSer LeuAlaAla AspGlySerPro GlyLeuLys SerValLeu  
 -----  
 701 GGAAGACCCC AGTGAAGCCA AAGAGAACCT CATTGCAA GAAACATCTG TGATAGAGTC GCTGGCTGCA GATGGAGCC CAGGGCTAAA ATCAGTGTCTA  
 CCTTCTGGG TCACITCGGT TTCTCTTGA GTAAGAGGT CTTTGTAGAC ACTATCTCAG CGACCCAGCT CTACCCCTCG GTCCCGATTT TAGTCACGAT

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## FIG. 1B

+3 SerThrSerArg AsnAsnCys AspThrGlyGlu LysProVal ValThrPhe LysGluAsnIle LysThrArg GluValAsn ArgAspGlnGly  
 801 TCACAAAGCC GAAATTAAAG CAACAACCTGT GACACAGGAG AGAAGCCAGT GGTACCTTC AAAGAAACA TTAAGACACG AGAAGTGAAC AGAGACCAAG  
 AGATGTTCCG CTTTAAATTC GTGTGTGACA CTGTGTCTC TCTTCGGICA CCAATGGAAG TTCTTTTGT AATCTGTGC TCTTCACTTG TCTCTGGTTC  
 +3 GlyArgSerPhe ProProLys GluValArgArg AspTyrSer LysGlyIle ThrValThrLys AsnAspGly LysLysAsp AsnAsnLysArg LysThrGlu  
 901 GAAGAAGTTT TCCTCCCAA GAGGTGAGAA GGGACTATAG CAAGGAATA ACTGTAACTA AGAATGATGG AAAGAAGGAC AACAAACAGA GGAATACTGA  
 CTTCTTCAA AGGAGGGTTT CTCCTACTTC CCCTGATATC GTTTCCTTAT TGACATTGAT TCTTACTACC TTTCTTCTTG TTGTTGTCT CTTTGTGACT  
 +3 GluThrLysLys CysThrLeuGlu LysLeuGln GluThrGly LysGlnAsnVal AlaValGln ValLysSer GlnThrGluLeu ArgLysThr ProValSer  
 1001 AACCAAGAA TGCACCTTAG AAAAGTTACA GGAACAGGA AGCAGAAATG TGGCAGTGCA GGTAAATCC CAGACAGAAC TAAGAAAGAC TCCAGTGTCT  
 TTGTTTCTTT ACGTGAATC TTTTCAATGT CTTTGTCTT CTTGCTCTAC ACCGTACAGT CCATTTTAGG GTCTGTCTTG ATTCTTTCTG AGGTACACAGA  
 +3 GluAlaArgLys ThrProVal ThrGlnThr ProThrGlnAla SerAsnSer GlnPheIle ProIleHisHis ProGlyAla PheProPro LeuProSerArg  
 1101 GAACCAGAA AACACCTGT AACTCAAACC CCACTCAAG CAAGTACTC CCAGTTCATC ACCCTGGAGC CTTCCTCTCT CTTCCACAGA  
 CTTCCGTCTT TTTGTGGACA TTGAGTTTGG GGTGAGTTTC GTTCATTGAG GGTCAAGTAG GGTAAAGTAG TGGACCTCG GAAGGGAGGA GAAGGTCTGT  
 +3 ArgProGlyPhe ProProPro ThrTyrValIle ProProPro ValAlaPhe SerMetGlySer GlyTyrThr PheProAla GlyValSerVal ProGlyThr  
 1201 GGCCAGGTT TCCGCCCCCA ACATATGTTA TCCCCCGCC TGTGGCATTT TCTATGGGT CAGTTACAC CTTCCAGCT GGTGTTTCTG TCCCAGGAAC  
 CCGTCCCAA AGGCGGGGT TGTATACAAT AGGCGGGCGG ACACCGTAAA AGATACCGGA GTCCAATGTG GAAGGTCTGA CCACAAAGAC AGGTCTCTTG  
 +3 ThrPheLeuGln ProThrAlaHis SerProAla GlyAsnGln ValGlnAlaGly LysGlnSer HisIlePro TyrSerGlnGln ArgProSer GlyProGly  
 1301 CTTTCTTCAG CCTACAGCTC ACTCTCCAGC AGGAACACAG GTGCAAGCTG GGAACAGTC CCACATTCTT TACAGCCAGC AACGGCCCTC TGGACCAAGG  
 GAAGAAGTC GGATGTGAG TGAGAGGTCTG TCCTTTGGTC CAGTTCGAC CTTTGTCTAG GGTGTAAGGA ATGTGCTGTC TTGCCGGGAG ACCTGTCTCC  
 +3 ProMetAsnGln GlyProGln GlnSerGln ProProSerGln GlnProLeu ThrSerLeu ProAlaGlnPro ThrAlaGln SerThrSer GlnLeuGlnVal  
 1401 CCAATGAACC AGGACCTCA ACAATCACAG CCACCTTCCC AGCAACCCCT TACATCTTTA CCAGCTCAGC CAACAGCACA GTCTACAAGC CAGCTGCAGG  
 GGTACTTGG TCCCTGGAGT TGTAGTGTG GGTGAAGGG TCGTTGGGA ATGTAGAAAT GGTGAGTCTG GTTGTCTGT CAGATGTTCTG GTCCAGCTCC

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## FIG. 1C

+3 ValGlnAlaLeu ThrGlnGln GlnGlnSerPro ThrLysAla ValProAla LeuGlyLysSer ProProHis HisSerGly PheGlnGlnTyr GlnGlnAla  
 -----  
 1501 TTCAAGCTCT AACTCAGCAA CAACAATCCC CTACAAAGC TGTGCCGGCT TTGGGAAAA GCCCGCTCA CCACTCTGGA TTCCAGCAGT ATCAACAGGC  
 AAGTTCGAGA TTGAGTCGTT GTTGTTAGGG GATGTTTTCG ACACGGCCGA AACCCCTTTT CGGGCGGAGT GGTGAGACCT AAGTTCGTCA TAGTTGTCCG  
 -----  
 +3 AlaAspAlaSer LysGlnLeuTyr AsnProPro GlnValGln GlyProLeuGly LysIleMet ProValLys GlnProTyrTyr LeuGlnThr GlnAspPro  
 -----  
 6001 AGATGCCCTCC AAACAGCTGT GGAATCCCC TCAGGTCAA GGTCCATTAG GGAATATTAT GCCTGTGAAA CAGCCCTACT ACCTTCAGAC CCAGACCCCC  
 TCTACGGAGG TTTGTTCGACA CCTTAGGGGG AGTCCAGTT CCAGGTAATC CCTTTTAATA CGACACATTT GTCCGGATGA TGGAACTCTG GGTTCCTGGG  
 -----  
 +3 IleLysLeuPhe GluProSer LeuGlnPro ProValMetGln GlnGlnPro LeuGluLys LysMetLysPro PheProMet GluProTyr AsnHisAsnPro  
 -----  
 1501 ATAAACTGT TTGAGCGGTC ATTGCAACCT CCTGTAAATG AGCAGCAGCC TCTAGAAAA AAATGAAGC CTTTTCCTCAT GGAGCCATAT AACCATATC  
 TATTTTGACA AACTCGCAG TAACGTGGA GGACATFACG TCGTCGTCCG AGATCTTTT TTTTACTTCG GAAAAGGTA CCTCGGTATA TTGTTATTAG  
 -----  
 +3 ProSerGluVal LysValPro GluPheTyrTrp AspSerSer TyrSerMet AlaAspAsnArg SerValMet AlaGlnGln AlaAsnIleAsp ArgArgGly  
 -----  
 1501 CCTCAGAAGT CAAGGTCCCA GAATCTTACT GGGATTCTTC CTACAGCATG GCTGTGTAAT GGCACAGCAA GCAAACATAG ACCGACAGGG  
 GGAGTCTTCA GTTCCAGGT CTTAAGATGA CCTAAGAAG GATGCTGTAC CGACTATTGT CTAGACATTA CCGTGTCTGT GGTTCGTATC TGGCGTCCCC  
 -----  
 +3 GlyLysArgSer ProGlyValPhe ArgProGlu GlnAspPro ValProArgMet ProPheGlu LysSerLeu LeuGluLysPro SerGluLeu MetSerHis  
 -----  
 1501 CAACGGTCA CCAGGATCT TCCGTCCAGA GCAGGATCCT GTACCCAGAA TGCCGTTTGA GAAATCCTTA TTGGAGAAGC CCTCAGAGCT CATGTCACAT  
 GTTTGCCAGT GGTCCCTCAGA AGGCAGGTCT CGTCTTAGGA CATGGGTCTT ACGGCAAACT CTTTAGGAAT AACCTCTTCG GGAGTCTCGA GTACAGTGTA  
 -----  
 +3 SerSerSerPhe LeuSerLeu ThrGlyPhe SerLeuAsnGln GluArgTyr ProAsnAsn SerMetPheAsn GluValTyr GlyLysAsn LeuThrSerSer  
 -----  
 2001 TCATCTCTCT TCCTGTCCCT CACGGGATTC TCTCTCAATC AGGAAGATA CCCAATAAT AGTATGTTCA ATGAGGTATA TGGGAAAAAC CTGACATCCA  
 AGTAGAGAA AGGACAGGA GTGGCCTAAG AGAGAGTTAG TCCTTTCTAT GGGTTTANTA TCATACAAGT TACTCCATAT ACCCTTTTTC GACTGTAGGT  
 -----  
 +3 SerSerLysAla GluLeuSer ProSerMetAla ProGlnGlu ThrSerLeu TyrSerLeuPhe GluGlyThr ProTrpSer ProSerLeuPro AlaSerSer  
 -----  
 2101 GCTCCAAAGC AGAATCAGT CCTCAATGG CCCCCAGGA AACATCTCTG TATTCCTTT TTGAAGGGAC TCCGTGCTCT CCATCACTTC CTGCCAGTTC  
 CGAGGTTTCG TCTTGAGTCA GGGAGTTACC GGGGGGTCTT TTGTAGAGAC ATAAGGAAA AACTTCCCTG AGGCACCAGA GGTAGTGAAG GACGTCGAAG

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## FIG. 1D

+3 SerAspHisSer ThrProAlaSer GlnSerPro HisSerSer AsnProSerSer LeuProSer SerProPro ThrHisAsnHis AsnSerVal PropheSer  
 -----  
 2201 AGATCATTCACACAGCCCA GCCAGTCTCC TCATTCCTCT AACCACAGCA GCCTACCCAG CTCTCTCTCCA ACACACAACC ATAATTCGT TCATTCCTCC  
 TCTAGTAAGT TGTGTCGGT CGGTCAGAGG AGTAAGGAGA TTGGGTTCTG CCGATGGGTC GAGAGGAGGT TGTTGTGTTGG TATTAAGACA AGGTAAGAGG  
 -----  
 +3 AsnPheGlyPro IleGlyThr ProAspAsn ArgAspArgArg ThrAlaAsp ArgTrpLys ThrAspLysPro AlaMetGly GlyPheGly IleAspTyrLeu  
 -----  
 2301 AATTTGGAC CCATTTGGAC TCCAGATAC AGGATAGAA GGACTGCAGA TCGGTGAAA ACTGATAAGC CAGCCATGGG TGGGTTGGC ATTGATTATC  
 TTAAACCTG GGTAAACCTG AGTCTATG TCCCTATCTT CCGTACGTCT AGCCACCTTT TGACTATCG GTCCGTACCC ACCCAACCG TAACTAATAG  
 -----  
 +3 LeuSerAlaThr SerSerSer GluSerSerTrp HisGlnAla SerThrPro SerGlyThrTrp ThrGlyHis GlyProSer MetGluAspSer SerAlaVal  
 -----  
 2401 TCTCAGCAAC GTCATCTCTT GAGAGCAGTT GGCATCAGGC CAGCACTCG AGTGGCACCT GGACAGGCCA TGGCCCTTCC ATGGAGGATT CCTCTGCTGT  
 AGAGTCGTTG CAGTAGGAGA CTCTCGTCAA CCGTAGTCCG GTCGTGAGSC TCACCGTGA CCTGTCCGTT ACCGGGAAGG TACCTCTCTAA GGAGACGACA  
 -----  
 +3 ValLeuMetGlu SerLeuLysSer IleTrpSer SerSerMet MethHisProGly ProSerAla LeuGluGln LeuLeuMetGln LysGlnGln  
 -----  
 2501 CCTCATGGAA AGCCTAAAGT CTATCTGGTC CAGTTCCATG ATGCATCTCG GACCTTCTGC TCTGGAGCAG CTGTTAATGC AGCAGAGCA GAAACAGCAA  
 GGAGTACCTT TCGGATTCA GATAGACCAG GTCAAGGTAC TACGTAGGAC CTGGAAGACG AGACCTCGTC GACAATTACG TCGTCTTCGT CTTGTGCTGT  
 -----  
 +3 ArgGlyGlnGly ThrMetAsn ProProHis \*\*\*  
 -----  
 2601 CCGGGACAAG GCACCATGAA CCTCCACAC TGAGGCAACT GTGGCAACT GGGATGAAG GCTCCATAAA CCATGGCATG TTGGGTTGC AGGACTGGCC  
 GCGCTGTTC CGTGTACTT GGGAGGTGTG ACTCGGTTT CACCGTTGA CCCTACTTC CGAGGTATTT GGTACCGTAC AACCCAAACG TCCTGACCCG  
 CACACAGTCC CCTGCAGGTG GCGCCCTCT TTTCTGTTT TCGCTGTCAA GAGGTGTAA GTATTCACCC AGCCCGCTGA GTGTGACGA AATGTTCCGA  
 GTGTGTGAGG GGACGTCCAC CGTCGGGAGA AAGACAAAG AGGACAGTT CTCCACATT CATAGGTGG TCGGCGGACT CACACGTGT TTACAAGCGT  
 GTGCAACAAA AAGAAAATC CATCAGGAAC TCTCCGTCCC CCGGGGGCT TCCGGAGGGA GAGAGAGAGG AACTGCTGTT TATCTCACTC AGTTACTTGG  
 CAGTTGTTT TTCTTTTITAG GTAGTCCTTG AGAGGCAGG GGGCCCCGGA AGGCTCTCC CTCTCTCTCC TTGACGACAA ATAGAGGTGAG TCAATGAACC  
 TATCACCGGC TCTCACC  
 ATAGTGGCGG AGAGTGG

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## FIG. 2A

1 ACCTGAGTAA GAGCTTGGAA AAGTTGAGCC CTCTTCGAGA GAAATTGGAA GAACAGTTTA AGAGGCTGCT ATTCCAAAAA GCTTCCAAT CTCAGCAGTT  
 TGGACACAGT TGCTGGCCCT CTTTATGTCT TTTCTTGGCA TCCTGTGCAA GTGTCTCTA CAGATGAGT CTCAGGAGGA GTCCTACAAAT GCCTATCCTC  
 101 ACCCTGTGCA ACGACCGGGA GAAATACAGA AAAGAACCGT AGGACACGTT CACAGGAGAT GTCTTACTCA GAGTCCTCCT CAGGATGTTA CGGATAGGAG  
 TCAAGTACAG TAACAGTAAT TGGACAAAGT TGAAGTAGTG GAAGCACTGA AATCGTTACT TTGGCTCGTC GTGTGAATAT CGGTTCTACT CGTCGATACA  
 MetSer PheLeuGlyIle LeuCysLys CysProLeu GlnAsnGluSer GlnGluGlu SerTyrAsn AlaTyrProLeu  
 -----  
 201 TGGACACAGT TGCTGGCCCT CTTTATGTCT TTTCTTGGCA TCCTGTGCAA GTGTCTCTA CAGATGAGT CTCAGGAGGA GTCCTACAAAT GCCTATCCTC  
 ACCCTGTGCA ACGACCGGGA GAAATACAGA AAAGAACCGT AGGACACGTT CACAGGAGAT GTCTTACTCA GAGTCCTCCT CAGGATGTTA CGGATAGGAG  
 LeuProAlaVal LysValSer MetAspTrpLeu ArgLeuArg ProArgVal PheGlnGluAla ValValAsp GluArgGln TyrIleTrpPro TrpLeuIle  
 -----  
 301 TTCCAGCAGT CAAGGTCCTC ATGACTGGC TAAGACTCAG ACCAGGGTC TTTCCAGGAG CAGTGGTGA TGAAGACAG TACATTTGGC CCGTGGTGTAT  
 AAGGTCGTCA GTTCCAGAG TACCTGACCG ATTCTGAGTC TGGGTCCCG AAGTCTCCG GTCAACCACT ACITTTCTGTC ATGTAAACCG GGACCAACTA  
 IleSerLeuLeu AsnSerPheHis ProHisGlu GluAspLeu SerSerIleSer AlaThrPro LeuProGlu GluPheGluLeu GlnGlyPhe LeuAlaLeu  
 -----  
 401 TTCTCTCTG AATAGTTTCC ATCCCATGA AGAGGACCTC TCAAGTATTA GTGCGACACC ACTTCCAGAG GAGTTTGAAT TACAAGGAT TTTGGCATTG  
 AAGAGAAGAC TTATCAAAGG TAGGGGTACT TCTCTGGAG AGTTCATAAT CACGCTGTGG TGAAGGTCTC CTCAAACTTA ATGTTCCCTAA AAACCGTAAC  
 ArgProSerPhe ArgAsnLeu AspPheSer LysGlyHisGln GlyIleThr GlyAspLys GluGlyGlnGln ArgArgIle ArgGlnGln ArgLeuIleSer  
 -----  
 501 AGACTTCTT TCAGGAACTT GGATTTTTC AAAGTCAACC AGGTATTAC AGGGGACAA GAAGGCCAGC AACGACGAAT ACGACAGCAA CGCTTGATCT  
 TCTGGAAGAA AGTCCTTGAA CCTAAAAAGG TTTCCAGTGG TCCATAANG TCCCTGTTT CTTCGGGTGG TTGCTGCTTA TGCTGTGCTT GCGAACTAGA  
 SerIleGlyLys TrpIleAla AspAsnGlnPro ArgLeuIle GlnCysGlu AsnGluValGly LysLeuLeu PheIleThr GluIleProGlu LeuIleLeu  
 -----  
 601 CTATAGGCAA ATGGAATTGCT GATAATCAGC CAAGGCTGAT TCAGTGTGAA AATGAGGTAG GGAATTTGTT GTTTATCACA GAAATCCAG AATTAATACT  
 GATATCCGTT TACCTRACGA CTATTAGTCG GTTCCGACTA AGTCACACTT TTAATCCATC CCTTTAACA CAAATAGTGT CTTAGGGTC TTAATATAGA  
 LeuGluAspPro SerGluAlaLys GluAsnLeu IleLeuGln GluThrSerVal IleGluSer LeuAlaAla AspGlySerPro GlyLeuLys SerValLeu  
 -----  
 701 GGAAGACCCC AGTGAAGCCA AAGAGAACCT CATTTGCAA GAAACATCTG TGATAGAGTC GTTGGCTGCA GATGGAGCC CAGGGCTAAA ATCAGTGCTA  
 CCTTCTGGG TCACTTCGGT TTCTCTTGA GTAAGCGTT CTTGTAGAC ACTATCTCAG  
 CAACCGACGT CTACCCCTGG GTCCCGATTT TAGTCACGAT

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## FIG. 2B

+3 SerThrSerArg AsnLeuSer AsnAsnCys AspThrGlyGlu LysProVal ValThrPhe LysGluAsnIle LysThrArg GluValAsn ArgAspGlnGly  
 TCTACAAGCC GAAATTTAAG CAACAACCTGC GACACAGGAG AGAAGCCAGT GGTACCTTC AAAGAAAACA TTAAGACACG AGAAGTGAC AGAGACCAAG  
 AGATGTTCCG CTTTAAATTC GTTGTGACG CTGTGTCCTC TCTTCGGTCA CCAATGGAAG TTCTTTTGT AATTCGTGTC TCTTCACTTG TCTCTGGTTC  
 +3 GlyArgSerPhe ProProLys GluValLysSer GlnThrGly LeuArgLys ThrProValSer GluAlaArg LysThrPro ValThrGlnThr ProThrGln  
 GAAGAAGTTT TCCTCCCAA GAGTAAAT CCCAGACAGG ACTAAGAAAG ACTCCAGTGT CTGAAGCCAG AAAACACCT GTAACCTCAA CCCCAACTCA  
 CTTCTTCAA AGGAGGGTTT CTCCATTITA GGTCTGTCC TGATCTTTC TGAGGTACA GACTTGGTC TTTTGTGGA CATTCAGTTT GGGGTGAGT  
 +3 GlnAlaSerAsn SerGlnPheIle ProIleHis HisProGly AlaPheProPro LeuProSer ArgProGly PheProProPro ThrTyrVal IleProPro  
 AGCAAGTAAC TCCAGTTCA TCCCATTTCA TCACCTTGA GCCTTCCCTC CTCTTCCAG CAGGCCAGG TTTCGCCCC CAACATATGT TATCCCCCGG  
 TCGTTCATTG AGGTCAGT AGGGTAAGT AGTGGACCT CGGAAGGGAG GAGAAGGTC GTCCGGTCC AAAGCGGG GTTGATACA ATAGGGGGG  
 +3 ProValAlaPhe SerMetGly SerGlyTyr ThrPheProAla GlyValSer ValProGly ThrPheLeuGln ProThrAla HisSerPro AlaGlyAsnGln  
 CCTGTGGCAT TTCTATGG CTGAGTTAC ACCTTCCAG CTGGTGTTC TGTCACGGA ACCTTCTTC AGCTACAGC TCACCTCCA GCAGAAACC  
 GGACACCGTA AAAGATACCC GATTCCAATG TGAAGGGTC GACCACAAAG ACAGGTCCT TGAAGAAG TCGGATGTC AGTGAGAGT CGTCTTTGG  
 +3 GlnValGlnAla GlyLysGln SerHisIlePro TyrSerGln GlnArgPro SerGlyProGly ProMetAsn GlnGlyPro GlnGlnSerGln ProProSer  
 AGGTGCAAGC TGGGAAACAG TCCACATTC CTTACAGCA GCAACGGCC TCTGGACCAG GGCCAAATGAA CCAGGACCT CAACAATCAC AGCCACCTTC  
 TCCAGTTTC ACCCTTTGTC AGGTGTAG GAATGTGCT CGTTGCCGG AGACTGCTC CCGTTACTT GGTCCCTGGA GTTGTAGTG TCGGTGGAAG  
 +3 SerGlnGlnPro LeuThrSerLeu ProAlaGln ProThrAla GlnSerThrSer GlnLeuGln ValGlnAla LeuThrGlnGln GlnGlnSer ProThrLys  
 CCAGCAACCC CTTACATCTT TACCAGCTCA GCCAACAGCA CAGTCTACAA GCCAGTGA GGTCAAGT CTAACCTCAGC AACAAATC CCCTACAAA  
 GGTCTGTTGG GAATGTAGAA ATGTCGAGT CCGTTGTCTGT GTGATGTT CCGTCCAGCT CCAAGTTTGA GATTGAGTCG TTGTTGTAG GGAATGTTT  
 +3 AlaValProAla LeuGlyLys SerProPro HisHisSerGly PheGlnGln TyrGlnGln AlaAspAlaSer LysGlnLeu TrpAsnPro ProGlnValGln  
 GCTGTGCCG CTTTGGGAA AAGCCCGCT CACCCTCTG GATTCAGCA GTATCCAGCA GTATCCAGT CCAACAGCT GTGAATCCC CCTCAGTTTC  
 CGACACGGCC GAAACCCCTT TTCGGGGCGA GTGGTGAGAC CTAAGTCTGT CATAGTTGTC CGTCTACGA GGTGTGTCGA CACCTTAGGG GGAGTCCAAG

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## FIG. 2C

+3 GlnGlyProLeu GlyLysile MetProVallys GlnProTyr TyrLeuGln ThrGlnAspPro IleLysLeu PheGluPro SerLeuGlnPro ProValMet  
 1501 AGGCCCAT AGGGAAAT ATGCTGTGA AACAGCCCTA CTACTTCAG ACCAAGACC CCATAAACT GTTGGCCG TCATTGCAAC CTCCTGTAAT  
 TTCCGGGTAA TCCCTTTTAA TACGACACT TTGTCGGAT GATGGAAGTC TGGGTCTGG GGTATTTTGA CAACTCGGC AGTAACGTTG GAGGACATTA  
 +3 MetGlnGlnGln ProLeuGluLys LysMetLys ProphePro MetGluProTyr AsnHisAsn ProSerGlu VallysValPro GluPheTyr TrpAspSer  
 1601 GCAGAGCAG CCTCTAGAAA AAAAATGAA GCCTTTTCCC ATGAGGCCAT ATAACATAA TCCTCAGAA GTCAGGTCC CAGAATTCTA CTGGATCTCT  
 CGTCGTCGTC GGAGATCTTT TTTTITACIT CGGAAAAGGG TACCTCGGTA TATTGGTATT AGGAGTCTT CAGTTCAGG GTCTTAAGAT GACCCTAAGA  
 +3 SerTyrSerMet AlaAspAsn ArgSerVal MetAlaGlnGln AlaAsnIle AspArgArg GlyLysArgSer ProGlyVal PheArgPro GluGlnAspPro  
 1701 TCCTACAGCA TGGCTGATAA CAGATCTGTA ATGGCACAAC AAGCAACAT AGACCGCAGG GGCAACGGT CAOCAGGAGT CTTCGGTCCA GAGCAGGATC  
 AGGATGTCGT ACGACTATT GTCTAGACAT TACCGTGTG TTCTTTTGTG TCTGGCTCC CGCTTTGCCA GTGCTCTCA GAAGGCAGGT CTGCTCCTAG  
 +3 ProValProArg MetProPhe GluLysSerLeu LeuGluLys ProSerGlu LeuMetSerHis SerSerSer PheLeuSer LeuThrGlyPhe SerLeuAsn  
 1801 CTGTACCCAG AATGCCGTTT GAGAAATCCT TATTGGAGAA GCCTTCAGAG CTCATGTCAC ATTCACTCTC TTTCCTGTCC CTCACOGGAT TCTCTCTCAA  
 GACATGGGTC TTACGGCAAA CTCCTTAGGA ATAACCTCTT CGGAGTCTC GAGTACAGTG TAAGTAGGAG AAAGGACAGG GAGTGGCCTA AGAGAGAGTT  
 +3 AsnGlnGluArg TyrProAsnAsn SerMetPhe AsnGluVal TyrGlyLysAsn LeuThrSer SerSerLys AlaGluLeuSer ProSerMet AlaProGln  
 1901 TCAGGAAGA TACCCAAATA ATAGTATGTT CAATGAGSTA TATGGGAAA ACCTGACATC CAGCTCCAAA GCAGAACTCA GTCCCTCAAT GGCCCCCAG  
 AGTCCTTCT ATGGGTTTAT TATCATACAA GTTACTCCAT ATACCCTTTT TGGACTGTAG GTGAGGTTT CGTCTTGAAT CAGGGAGTTA CCGGGGGGTC  
 +3 GluThrSerLeu TyrSerLeu PheGluGly ThrProTrpSer ProSerLeu ProAlaSer SerAspHisSer ThrProAla SerGlnSer ProHisSerSer  
 2001 GAAACATCTC TGTATTCCCT TTTTGAAGG ACTCCGTGTT CTCCATCACT TCCTGCCAGT TCAGATCAAT CAACACCAGC CAGCCAGTCT CCTCAATCCT  
 CTTTGTAGAG ACATAAGGA AAAACTTCCC TGAGGCACCA GAGGTAGTGA AGAAGGTCA AGTCTAGTAA GTTGTGTGCG GTGCTCAGA GGAGTAAGA  
 +3 SerAsnProSer SerLeuPro SerSerProPro ThrHisAsn HisAsnSer ValProPheSer AsnPheGly ProIleGly ThrProAspAsn ArgAspArg  
 2101 CTAACCCAAG CAGCCTACCC AGCTCTCTC CAACACAA CCAATATTCT GTTCCATCT ACCATTGG ACCATTGG ACTCCAGATA ACAGGATAG  
 GATTGGGTTG GTCGGATGG TCGAGAGGAG GTTGTGTGTT GGTATTAGA CAAGGTAAGA GGTAAACC TGGTAACCC TGAGGTCTAT TGTCCCTATC

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## FIG. 2D

+3 ArgArgThrAla AspArgTrpLys ThrAspLys ProAlaMet GlyGlyPheGly IleAspTyr LeuSerAla ThrSerSerSer GluSerSer TrpHisGln  
-----  
2201 AAGGACTGCA GATCGGTGGA AAACGTGATAA GCCAGCCCATG GGTGGGTTTG GCATTGATTA TCCTTCAGCA AGTCATCCT CTGAGAGCAG TTGGCATCAG  
TTCTTGACGT CTAGCCACCT TTTGACTATT CGGTGGGTAC CCACCAAAC CGTAACATAAT AGAGAGTCGT TGCAGTAGGA GACTCTCGTC AACCGTAGTC  
-----  
+3 AlaSerThrPro SerGlyThr TrpThrGly HisGlyProSer MetGluAsp SerSerAla ValLeuMetGlu SerLeuLys SerIleTrp SerSerSerMet  
-----  
301 GCCAGCACTC CGAGTGGCAC CTGGACAGGC CATGGCCCTT CCATGGAGGA TTCCTCTGCT GTCTTCATGG AAAGCCTAAA GTCTATCTGG TCCAGTTCCA  
CGGTCTGAG GCTCACCGTG GACCTGTCCG GTACCGGGAA GGTACTCTCT AAGGAGACCA CAGGAGTACC TTTCGGATTT CAGATAGACC AGGTCAAGGT  
-----  
+3 MetMetHisPro GlyProSer AlaLeuGluGln LeuLeuMet GlnGlnLys GlnLysGlnGln ArgGlyGln GlyThrMet AsnProProHis \*\*\*  
-----  
401 TGATGCATCC TGGACCTTCT GCTCTGGAGC AGCTGTTTAT GCAGCAGAAG CAGAAACAGC AACGGGGACA AGGCACCATG AACCTCCAC ACTGAGGCCA  
ACTACGTAGG ACCTGGAAGA CGAGACCTCG TCGACAATTA CGTCGTCTTC GTCTTTGTGCG TTGCCCCGTGT TCCGTGGTAC TTGGAGGTG TGACTCCGGT  
501 AAGTGGCAAC CTGGGAATGA AGGTCCATA AACCATGGCA TGTGGGTTT GCAGGACTGG CCGACACAGT CCCCTGCAGG TGGCAGCCCT CTTTCTCTGT  
TTACCCGTTG GACCCTTACT TCCGAGGTAT TGGTACCCT ACAACCCAAA CGTCCTGACC GGGTGTGTCA GGGGACGTCC ACCGTGGGA GAAAGACAA  
1501 TCTCGCTGTC AAGAGGTGT AAGTATTCCA CCAGCCCGCT GAGTGTGCAC GAAATGTTG CAGTCAACA AAAAGAAAAA TCCATCAGGA ACTCTCCGTC  
AGAGGCACAG TTCTCCACCA TTCATAAGGT GGTGGGGCGA CTCACACGTG CTTTACAAAG GTCAAGTTGT TTTCTTTT AGGTAGTCTT TGAGAGGCAG  
2701 CCCCCGGGC CTTCCGGAGG GAGAGAGAGA GGAAGTGTG TTTATCTCAC TCAGTTACTT GGTATCACCG CCTCTCAC  
GGGGGCCCCG GAAGGCCTCC CTCTCTCTCT CTTGACGAC AAATAGAGTG AGTCAATGAA CCATAGTGGC GGAGAGTGG

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FIG. 3

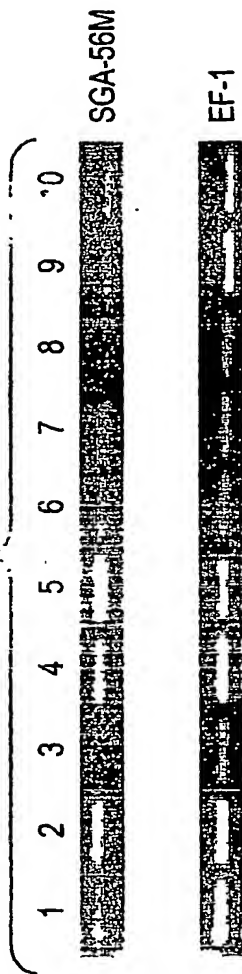
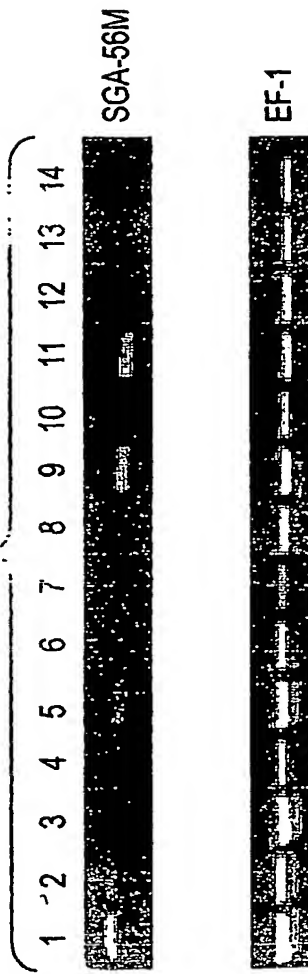


FIG. 4



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FIG. 5A

	1	2	3	4	5	6	7	8	9	10	11
A	•	•	•	•	•	•	•	•	•	•	•
B	•	•	•	•	•	•	•	•	•	•	•
C	•	•	•	•	•	•	•	•	•	•	•
D	•	•	•	•	•	•	•	•	•	•	•
E	•	•	•	•	•	•	•	•	•	•	•
F	•	•	•	•	•	•	•	•	•	•	•
G	•	•	•	•	•	•	•	•	•	•	•
H	•	•	•	•	•	•	•	•	•	•	•

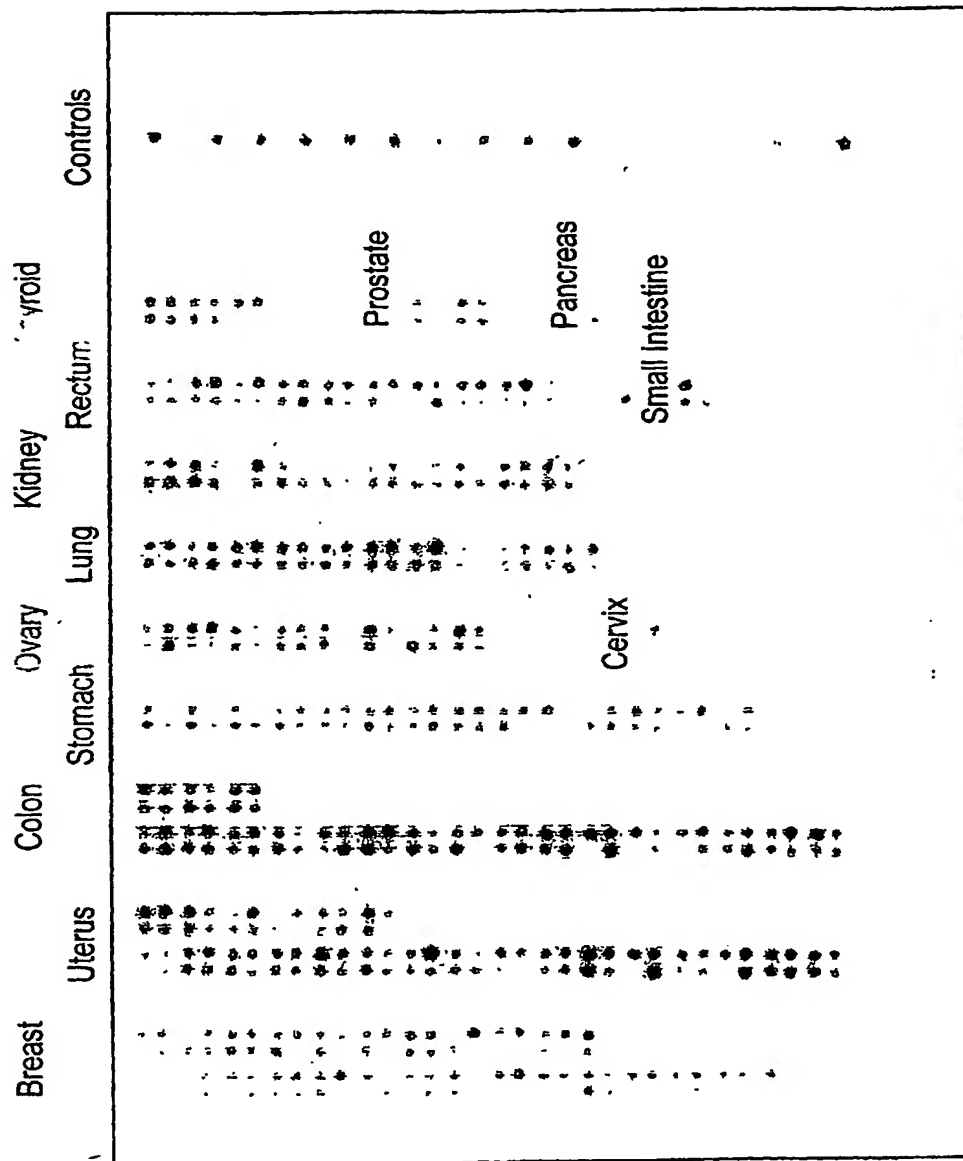
FIG. 5B

	1	2	3	4	5	6	7	8	9	10	11
A											
B											
C											
D											
E											
F											
G											
H											

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FIG. 6



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## FIG. 7

```

1  MSFLGILCKC PLQNESQEEES YNAYPLPAVK VSMDWLRLRP RVFQEAVVDE
51 RQYIWPWLIS LLNSFHPHEE DLSSISATPL PEEFELQGFL ALRPSFRNLD
101 FSKGHQGITG DKEGQQRIR QQRLLSIGKW IADNQPRLIQ CENEVGKLLF
151 ITEIPELILE DPSEAKENLI LQETSVIESL AADGSPGLKS VLSTSRNLSN
201 NCDTGEKPVV TFKENIKTRE VNRDQGRSFP PKEVRRDYSK GITVTKNDGK
251 KDNNKRKTET KKCTLEKLQE TGKQNVAVQV KSQTELKRTP VSEARKTPVT
301 QTPTQASNSQ FIPIHHPGAF PPLPSRPGFP PPTYVIPPP V AFMSGGYTF
351 PAGVSVPGTF LQPTAHSPAG NQVQAGKQSH IPYSQQRPSG PGPMNQGPQQ
401 SQPPSQQPLT SLPAQPTAQS TSQQLQVQALT QQQQSPTKAV PALGKSPPHH
451 SGFQQYQQAD ASKQLWNPPQ VQGPLGKIMP VKQPYYLQTQ DPIKLFEP SL
501 QPPVMQQQPL EKKMKFPFME PYNHNPSEVK VPEFYWDSSY SMADNRSVMA
551 QQANIDRRGK RSPGVFRPEQ DPVPRMPFEK SLLEKPSELM SHSSSFLSLT
601 GFSLNQERYP NNSMFNEVYG KNLTSSSKAE LSPSMAQET SLYSLFEGTP
651 WSPSLPASSD HSTPASQSPH SSNPSSLPSS PPTHNHNSVP FSNFGPIGTP
701 DNRDRRTADR WKTDKPAMGG FGIDYLSATS SSESSWHQAS TPSGTWTGHG
751 PSMEDSSAVL MESLKSIISS SMHHPGPSAL EQLLMQQKQK QQRGQGTMPN
801 PH

```

## FIG. 8

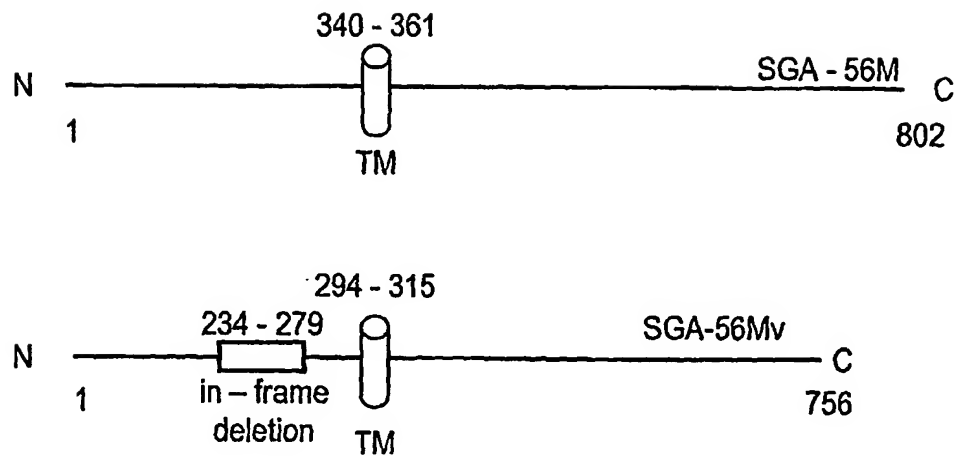
```

1  MSFLGILCKC PLQNESQEEES YNAYPLPAVK VSMDWLRLRP RVFQEAVVDE
51 RQYIWPWLIS LLNSFHPHEE DLSSISATPL PEEFELQGFL ALRPSFRNLD
101 FSKGHQGITG DKEGQQRIR QQRLLSIGKW IADNQPRLIQ CENEVGKLLF
151 ITEIPELILE DPSEAKENLI LQETSVIESL AADGSPGLKS VLSTSRNLSN
201 NCDTGEKPVV TFKENIKTRE VNRDQGRSFP PKEVKSQTGL RKTVPSEARK
251 TPVTQTPTQA SNSQFIPHH PGAFPPPSR PGFPPPTYVI PPPVAFMSG
301 GYTTPAGVSV PGTFLQPTAH SPAGNQVQAG KQSHIPYSQQ RPSGPGPMNQ
351 GPQQSQPPSQ QPLTSLPAQP TAQSTSQQLV QALTQQQQSP TKAVPALGKS
401 PPHHSGFQQY QQADASKQLW NPPQVQGPLG KIMPVKQPY LQTQDPIKLF
451 EPSLQPPVMQ QQPLEKKMKP FMEPYNHNP SEVKVPEFYW DSSYSMADNR
501 SVMAQQANID RRGKRSPGVF RPEQDPVPRM PFEKSLLEKP SELMSHSSSF
551 LSLTGFSLNQ ERYPNNSMFN EVYGKNLTSS SKAELSPSMA PQETSLYSLF
601 EGTPWSPSLP ASSDHSTPAS QSPHSSNPSS LPSSPPTHNH NSVPFSNFGP
651 IGTPDNRDRR TADRWKTDKP AMGGFGIDYL SATSSSESSW HQASTPSGTW
701 TGHGPSMEDS SAVLMESLKS IWSSSMHHPG PSALEQLLMQ QKQKQQRGQG
751 TMNPPH

```

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FIG. 9



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